



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Atty. Docket No: SALK1720-6

In re patent application of

MATHEWS, LAWRENCE S. *et al.*

Serial No. 09/742,684

Filed: December 19, 2000

For: CLONING AND RECOMBINANT PRODUCTION OF RECEPTOR(S) OF
THE ACTIVIN/TGF-BETA SUPERFAMILY

STATEMENT TO SUPPORT FILING AND SUBMISSION IN
ACCORDANCE WITH 37 C.F.R. §§ 1.821-1.825

RECEIVED

Assistant Commissioner for Patents
Washington, D.C. 20231
Box SEQUENCE

MAY 02 2003

TECH CENTER 1600/2900

Sir:

In connection with a Sequence Listing submitted concurrently
herewith, the undersigned hereby states that:

1. the submission, filed herewith in accordance with 37
C.F.R. § 1.821(g), does not include new matter;

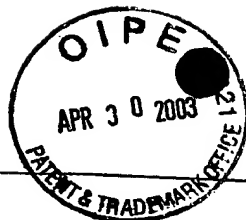
2. the content of the attached paper copy and the
attached computer readable copy of the Sequence Listing, submitted in
accordance with 37 C.F.R. § 1.821(c) and (e), respectively, are the same.

Respectfully submitted,

David M. Narkunas
Reg. No. 53,370

April 22, 2003
Date

HARBOR CONSULTING IP SERVICES, INC.
1500A Lafayette Road, #262
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800-318-3021



1

SEQUENCE LISTING

<110> MATHEWS, LAWRENCE S.
VALE JR., WYLIE W.
TSUCHIDA, KUNIHIRO

<120> CLONING AND RECOMBINANT PRODUCTION OF RECEPTOR(S) OF
THE ACTIVIN/TGF-BETA SUPERFAMILY

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MAY 02 2003

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 <212> PRT
 <213> Homo sapiens

<400> 8
 Gly Thr Arg Arg Tyr Met
 1 5

<210> 9
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Consensus
 sequence

<400> 9
 Asp Leu Ala Ala Arg Asn
 1 5

<210> 10
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Consensus
 sequence

<220>
 <221> MOD_RES
 <222> (1)
 <223> Variable amino acid

<220>
 <221> MOD_RES

<222> (3)
 <223> Ile or Val

<220>
 <221> MOD_RES
 <222> (4)
 <223> Lys or Arg

<220>
 <221> MOD_RES
 <222> (6)
 <223> Thr or Met

<400> 10
 Xaa Pro Xaa Xaa Trp Xaa
 1 5

<210> 11
 <211> 1602
 <212> DNA
 <213> Rattus sp.

<220>
 <221> CDS
 <222> (72)..(1550)

<400> 11
 ccccggaac ttcaaagcgc gctgcggcgg cgctctggga ccccgaaagcc ttgcaccgcc 60
 gcgggggtggc c atg acc cca gcg cgc cgc tcc gca ctg agc ctg gcc ctc 110
 Met Thr Pro Ala Arg Arg Ser Ala Leu Ser Leu Ala Leu
 1 5 10
 ctg ctg gtg gca ctg gcc tcc gac ctt gcg gca gga ctg aag tgt gtg 158
 Leu Leu Val Ala Leu Ala Ser Asp Leu Ala Ala Gly Leu Lys Cys Val
 15 20 25
 tgt ctt ttg tgt gat tcc tca aac ttt acc tgc caa acc gaa gga gca 206
 Cys Leu Leu Cys Asp Ser Ser Asn Phe Thr Cys Gln Thr Glu Gly Ala
 30 35 40 45
 tgc tgg gcc tct gtc atg cta acc aac ggg aaa gaa cag gtg agc aaa 254
 Cys Trp Ala Ser Val Met Leu Thr Asn Gly Lys Glu Gln Val Ser Lys
 50 55 60
 tcg tgc gtg tcc ctc ccg gaa cta aat gct cag gtc ttc tgt cac agt 302
 Ser Cys Val Ser Leu Pro Glu Leu Asn Ala Gln Val Phe Cys His Ser
 65 70 75
 tcc aac aac gtg acc aag acc gaa tgt tgc ttc aca gac ttc tgc aac 350
 Ser Asn Asn Val Thr Lys Thr Glu Cys Cys Phe Thr Asp Phe Cys Asn
 80 85 90
 aac atc act cag cac ctt ccc aca gca tct cca gat gcc cct aga ctt 398
 Asn Ile Thr Gln His Leu Pro Thr Ala Ser Pro Asp Ala Pro Arg Leu
 95 100 105

ggc ccc aca gag ctg aca gtt gtt atc act gta cct gtt tgc ctc ctg	446
Gly Pro Thr Glu Leu Thr Val Val Ile Thr Val Pro Val Cys Leu Leu	
110 115 120 125	
tcc atc gca gcc atg cta acg ata tgg gcc tgc cag gac cgc cag tgc	494
Ser Ile Ala Ala Met Leu Thr Ile Trp Ala Cys Gln Asp Arg Gln Cys	
130 135 140	
aca tac agg aag acc aag aga cac aat gtg gag gaa cca ctg gca gag	542
Thr Tyr Arg Lys Thr Lys Arg His Asn Val Glu Glu Pro Leu Ala Glu	
145 150 155	
tac agc ctt gtc aat gct gga aaa acc ctc aaa gat ctg att tat gat	590
Tyr Ser Leu Val Asn Ala Gly Lys Thr Leu Lys Asp Leu Ile Tyr Asp	
160 165 170	
gcc act gcc tcg ggc tca gga tct ggc ccg cct ctt ttg gtt caa aga	638
Ala Thr Ala Ser Gly Ser Gly Ser Gly Pro Pro Leu Leu Val Gln Arg	
175 180 185	
acc atc gca agg aca att gta ctt caa gaa atc gta gga aaa ggt cgg	686
Thr Ile Ala Arg Thr Ile Val Leu Gln Glu Ile Val Gly Lys Gly Arg	
190 195 200 205	
ttt ggg gaa gtg tgg cac gga aga tgg tgt gga gaa gat gtg gct gtg	734
Phe Gly Glu Val Trp His Gly Arg Trp Cys Gly Glu Asp Val Ala Val	
210 215 220	
aaa ata ttc tcc tcc aga gat gag aga tct tgg ttc cgt gag gca gaa	782
Lys Ile Phe Ser Ser Arg Asp Glu Arg Ser Trp Phe Arg Glu Ala Glu	
225 230 235	
att tat cag acg gta atg ctg aga cat gag aat att ctc ggt ttc atc	830
Ile Tyr Gln Thr Val Met Leu Arg His Glu Asn Ile Leu Gly Phe Ile	
240 245 250	
gcg gcc gac aac aaa gat aat gga acc tgg act cag ctt tgg ctt gtg	878
Ala Ala Asp Asn Lys Asp Asn Gly Thr Trp Thr Gln Leu Trp Leu Val	
255 260 265	
tca gag tat cac gag cag ggc tcc tta tat gac tat ttg aat aga aac	926
Ser Glu Tyr His Glu Gln Gly Ser Leu Tyr Asp Tyr Leu Asn Arg Asn	
270 275 280 285	
ata gtg acc gtg gct gga atg gtc aag ttg gcg ctt tca ata gcg agt	974
Ile Val Thr Val Ala Gly Met Val Lys Leu Ala Leu Ser Ile Ala Ser	
290 295 300	
ggt ctg gct cac cta cac atg gag atc gtg ggc act caa ggt aag cct	1022
Gly Leu Ala His Leu His Met Glu Ile Val Gly Thr Gln Gly Lys Pro	
305 310 315	
gct att gct cac cga gat ata aag tca aag aat atc tta gtc aaa aag	1070
Ala Ile Ala His Arg Asp Ile Lys Ser Lys Asn Ile Leu Val Lys Lys	
320 325 330	

tgt gac act tgt gcc ata gct gac tta ggg ctg gct gtg aaa cat gat 1118
 Cys Asp Thr Cys Ala Ile Ala Asp Leu Gly Leu Ala Val Lys His Asp
 335 340 345

tct atc atg aac act ata gat ata ccc cag aat cct aaa gtg gga acc 1166
 Ser Ile Met Asn Thr Ile Asp Ile Pro Gln Asn Pro Lys Val Gly Thr
 350 355 360 365

aag agg tat atg gct ccc gaa atg ctt gat gat aca atg aac gtc aac 1214
 Lys Arg Tyr Met Ala Pro Glu Met Leu Asp Asp Thr Met Asn Val Asn
 370 375 380

atc ttt gag tcc ttc aag cga gct gac atc tat tcg gtg ggg ctg gtt 1262
 Ile Phe Glu Ser Phe Lys Arg Ala Asp Ile Tyr Ser Val Gly Leu Val
 385 390 395

tac tgg gaa ata gct cga agg tgt tca gtt gga gga ctt gtt gaa gag 1310
 Tyr Trp Glu Ile Ala Arg Arg Cys Ser Val Gly Gly Leu Val Glu Glu
 400 405 410

tac cag ttg cct tat tat gac atg gtg cct tca gat cct tcc ata gag 1358
 Tyr Gln Leu Pro Tyr Tyr Asp Met Val Pro Ser Asp Pro Ser Ile Glu
 415 420 425

gaa atg agg aag gtc gtt tgt gat cag aaa ctg cga cca aat ctc cca 1406
 Glu Met Arg Lys Val Val Cys Asp Gln Lys Leu Arg Pro Asn Leu Pro
 430 435 440 445

aac cag tgg caa agc tgt gag gcg ctc cgg gtc atg gga aga ata atg 1454
 Asn Gln Trp Gln Ser Cys Glu Ala Leu Arg Val Met Gly Arg Ile Met
 450 455 460

cgt gag tgc tgg tat gcc aac ggg gca gct cgc ctg acc gcc ctg cgc 1502
 Arg Glu Cys Trp Tyr Ala Asn Gly Ala Ala Arg Leu Thr Ala Leu Arg
 465 470 475

gtg aag aag acc att tct cag ctg tgt gtc aag gaa gac tgt aag gcc 1550
 Val Lys Lys Thr Ile Ser Gln Leu Cys Val Lys Glu Asp Cys Lys Ala
 480 485 490

taaggataca ggcgacggga aagccctcac cactctcttt catgtctcct gc 1602

<210> 12

<211> 493

<212> PRT

<213> Rattus sp.

<400> 12

Met Thr Pro Ala Arg Arg Ser Ala Leu Ser Leu Ala Leu Leu Leu Val
1 5 10 15

Ala Leu Ala Ser Asp Leu Ala Ala Gly Leu Lys Cys Val Cys Leu Leu
20 25 30

Cys Asp Ser Ser Asn Phe Thr Cys Gln Thr Glu Gly Ala Cys Trp Ala
35 40 45

Ser Val Met Leu Thr Asn Gly Lys Glu Gln Val Ser Lys Ser Cys Val
 50 55 60
 Ser Leu Pro Glu Leu Asn Ala Gln Val Phe Cys His Ser Ser Asn Asn
 65 70 75 80
 Val Thr Lys Thr Glu Cys Cys Phe Thr Asp Phe Cys Asn Asn Ile Thr
 85 90 95
 Gln His Leu Pro Thr Ala Ser Pro Asp Ala Pro Arg Leu Gly Pro Thr
 100 105 110
 Glu Leu Thr Val Val Ile Thr Val Pro Val Cys Leu Leu Ser Ile Ala
 115 120 125
 Ala Met Leu Thr Ile Trp Ala Cys Gln Asp Arg Gln Cys Thr Tyr Arg
 130 135 140
 Lys Thr Lys Arg His Asn Val Glu Glu Pro Leu Ala Glu Tyr Ser Leu
 145 150 155 160
 Val Asn Ala Gly Lys Thr Leu Lys Asp Leu Ile Tyr Asp Ala Thr Ala
 165 170 175
 Ser Gly Ser Gly Ser Gly Pro Pro Leu Leu Val Gln Arg Thr Ile Ala
 180 185 190
 Arg Thr Ile Val Leu Gln Glu Ile Val Gly Lys Gly Arg Phe Gly Glu
 195 200 205
 Val Trp His Gly Arg Trp Cys Gly Glu Asp Val Ala Val Lys Ile Phe
 210 215 220
 Ser Ser Arg Asp Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln
 225 230 235 240
 Thr Val Met Leu Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp
 245 250 255
 Asn Lys Asp Asn Gly Thr Trp Thr Gln Leu Trp Leu Val Ser Glu Tyr
 260 265 270
 His Glu Gln Gly Ser Leu Tyr Asp Tyr Leu Asn Arg Asn Ile Val Thr
 275 280 285
 Val Ala Gly Met Val Lys Leu Ala Leu Ser Ile Ala Ser Gly Leu Ala
 290 295 300
 His Leu His Met Glu Ile Val Gly Thr Gln Gly Lys Pro Ala Ile Ala
 305 310 315 320
 His Arg Asp Ile Lys Ser Lys Asn Ile Leu Val Lys Lys Cys Asp Thr
 325 330 335
 Cys Ala Ile Ala Asp Leu Gly Leu Ala Val Lys His Asp Ser Ile Met
 340 345 350

Asn Thr Ile Asp Ile Pro Gln Asn Pro Lys Val Gly Thr Lys Arg Tyr
 355 360 365
 Met Ala Pro Glu Met Leu Asp Asp Thr Met Asn Val Asn Ile Phe Glu
 370 375 380
 Ser Phe Lys Arg Ala Asp Ile Tyr Ser Val Gly Leu Val Tyr Trp Glu
 385 390 395 400
 Ile Ala Arg Arg Cys Ser Val Gly Gly Leu Val Glu Glu Tyr Gln Leu
 405 410 415
 Pro Tyr Tyr Asp Met Val Pro Ser Asp Pro Ser Ile Glu Glu Met Arg
 420 425 430
 Lys Val Val Cys Asp Gln Lys Leu Arg Pro Asn Leu Pro Asn Gln Trp
 435 440 445
 Gln Ser Cys Glu Ala Leu Arg Val Met Gly Arg Ile Met Arg Glu Cys
 450 455 460
 Trp Tyr Ala Asn Gly Ala Ala Arg Leu Thr Ala Leu Arg Val Lys Lys
 465 470 475 480
 Thr Ile Ser Gln Leu Cys Val Lys Glu Asp Cys Lys Ala
 485 490

<210> 13
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<220>
 <221> modified_base
 <222> (11)
 <223> a, t, c or g

<220>
 <221> modified_base
 <222> (14)
 <223> a, t, c or g

<220>
 <221> modified_base
 <222> (17)
 <223> a, t, c or g

<400> 13
 cgggatccgt ngcngtnaar athttycc

<210> 14
 <211> 35

<212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<220>
 <221> modified_base
 <222> (12)
 <223> a, t, c or g

<220>
 <221> modified_base
 <222> (15)
 <223> a, t, c or g

<220>
 <221> modified_base
 <222> (24)
 <223> a, t, c or g

<220>
 <221> modified_base
 <222> (30)
 <223> a, t, c or g

<220>
 <221> modified_base
 <222> (33)
 <223> a, t, c or g

<400> 14
 cgggatccyt cnggngccat rtanckycn gtncc

35

<210> 15
 <211> 2563
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (71)..(1609)

<220>
 <221> modified_base
 <222> (346)
 <223> a, t, c or g

<400> 15
 ctccgaggaa gaccagggga actggatatc tagcgagaac ttctacggc ttctccggcg 60

cctcgggaaa atg gga gct gct gca aag ttg gcg ttc gcc gtc ttt ctt 109
 Met Gly Ala Ala Ala Lys Leu Ala Phe Ala Val Phe Leu
 1 5 10

atc tct tgc tct tca ggt gct ata ctt ggc aga tca gaa act cag gag	157
Ile Ser Cys Ser Ser Gly Ala Ile Leu Gly Arg Ser Glu Thr Gln Glu	
15 20 25	
tgt ctt ttc ttt aat gct aat tgg gaa aar gac aga acc aac cag act	205
Cys Leu Phe Phe Asn Ala Asn Trp Glu Lys Asp Arg Thr Asn Gln Thr	
30 35 40 45	
ggt gtt gaa cct tgc tat ggt gat aaa gat aaa cgg cga cat tgt ttt	253
Gly Val Glu Pro Cys Tyr Gly Asp Lys Asp Lys Arg Arg His Cys Phe	
50 55 60	
gct acc tgg aag aat att tct ggt tcc att gaa ata gtg aag caa ggt	301
Ala Thr Trp Lys Asn Ile Ser Gly Ser Ile Glu Ile Val Lys Gln Gly	
65 70 75	
tgt tgg ctg gat gat atc aac tgc tat gac agg act gat tgt gtn gaa	349
Cys Trp Leu Asp Asp Ile Asn Cys Tyr Asp Arg Thr Asp Cys Val Glu	
80 85 90	
aaa aaa gac agc cct gaa gtg tac ttt tgt tgc tgt gag ggc aat atg	397
Lys Lys Asp Ser Pro Glu Val Tyr Phe Cys Cys Cys Glu Gly Asn Met	
95 100 105	
tgt aat gaa aag ttc tct tat ttt ccg gag atg gaa gtc aca cag ccc	445
Cys Asn Glu Lys Phe Ser Tyr Phe Pro Glu Met Glu Val Thr Gln Pro	
110 115 120 125	
act tca aat cct gtt aca ccg aag cca ccc tat tac aac att ctg ctg	493
Thr Ser Asn Pro Val Thr Pro Lys Pro Pro Tyr Tyr Asn Ile Leu Leu	
130 135 140	
tat tcc ttg gta cca cta atg tta att gca gga att gtc att tgt gca	541
Tyr Ser Leu Val Pro Leu Met Leu Ile Ala Gly Ile Val Ile Cys Ala	
145 150 155	
ttt tgg gtg tac aga cat cac aag atg gcc tac cct cct gta ctt gtt	589
Phe Trp Val Tyr Arg His His Lys Met Ala Tyr Pro Pro Val Leu Val	
160 165 170	
cct act caa gac cca gga cca ccc cca cct tcc cca tta cta ggg ttg	637
Pro Thr Gln Asp Pro Gly Pro Pro Pro Pro Ser Pro Leu Leu Gly Leu	
175 180 185	
aag cca ttg cag ctg tta gaa gtg aaa gca agg gga aga ttt ggt tgt	685
Lys Pro Leu Gln Leu Leu Glu Val Lys Ala Arg Gly Arg Phe Gly Cys	
190 195 200 205	
gtc tgg aaa gcc cag ttg ctc aat gaa tat gtg gct gtc aaa ata ttt	733
Val Trp Lys Ala Gln Leu Leu Asn Glu Tyr Val Ala Val Lys Ile Phe	
210 215 220	
cca ata cag gac aaa cag tcc tgg cag aat gaa tat gaa gtc tat agt	781
Pro Ile Gln Asp Lys Gln Ser Trp Gln Asn Glu Tyr Glu Val Tyr Ser	
225 230 235	

cta cct gga atg aag cat gag aac ata cta cag ttc att ggt gca gag	829
Leu Pro Gly Met Lys His Glu Asn Ile Leu Gln Phe Ile Gly Ala Glu	
240 245 250	
aaa aga ggc acc agt gtg gat gtg gac ctg tgg cta atc aca gca ttt	877
Lys Arg Gly Thr Ser Val Asp Val Asp Leu Trp Leu Ile Thr Ala Phe	
255 260 265	
cat gaa aag ggc tca ctg tca gac ttt ctt aag gct aat gtg gtc tct	925
His Glu Lys Gly Ser Leu Ser Asp Phe Leu Lys Ala Asn Val Val Ser	
270 275 280 285	
tgg aat car ctt tgt cat att gca gaa acc atg gct aga gga ttg gca	973
Trp Asn Gln Leu Cys His Ile Ala Glu Thr Met Ala Arg Gly Leu Ala	
290 295 300	
tat tta cat gag gat ata cct ggc tta aaa gat ggc cac aag cct gca	1021
Tyr Leu His Glu Asp Ile Pro Gly Leu Lys Asp Gly His Lys Pro Ala	
305 310 315	
atc tct cac agg gac atc aaa agt aaa aat gtg ctg ttg aaa aac aat	1069
Ile Ser His Arg Asp Ile Lys Ser Lys Asn Val Leu Leu Lys Asn Asn	
320 325 330	
ctg aca gct tgc att gct gac ttt ggg ttg gcc tta aag ttc gag gct	1117
Leu Thr Ala Cys Ile Ala Asp Phe Gly Leu Ala Leu Lys Phe Glu Ala	
335 340 345	
ggc aag tct gca ggt gac acc cat ggg cag gtt ggt acc cgg agg tat	1165
Gly Lys Ser Ala Gly Asp Thr His Gly Gln Val Gly Thr Arg Arg Tyr	
350 355 360 365	
atg gct cca gag gtg ttg gag ggt gct ata aac ttc caa agg gac gca	1213
Met Ala Pro Glu Val Leu Glu Gly Ala Ile Asn Phe Gln Arg Asp Ala	
370 375 380	
ttt ctg agg ata gat atg tac gcc atg gga tta gtc cta tgg gaa ttg	1261
Phe Leu Arg Ile Asp Met Tyr Ala Met Gly Leu Val Leu Trp Glu Leu	
385 390 395	
gct tct cgt tgc act gct gca gat gga ccc gta gat gag tac atg tta	1309
Ala Ser Arg Cys Thr Ala Ala Asp Gly Pro Val Asp Glu Tyr Met Leu	
400 405 410	
cca ttt gag gaa gaa att ggc cag cat cca tct ctt gaa gat atg cag	1357
Pro Phe Glu Glu Glu Ile Gly Gln His Pro Ser Leu Glu Asp Met Gln	
415 420 425	
gaa gtt gtt gtg cat aaa aaa aag agg cct gtt tta aga gat tat tgg	1405
Glu Val Val Val His Lys Lys Lys Arg Pro Val Leu Arg Asp Tyr Trp	
430 435 440 445	
cag aaa cat gca gga atg gca atg ctc tgt gaa acg ata gaa gaa tgt	1453
Gln Lys His Ala Gly Met Ala Met Leu Cys Glu Thr Ile Glu Glu Cys	
450 455 460	

tgg gat cat	gat gca gaa gcc agg tta tca gct gga tgt gta ggt gaa	1501
Trp Asp His	Asp Ala Glu Ala Arg Leu Ser Ala Gly Cys Val Gly Glu	
	465	470
		475

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aga att act cag atg caa aga cta aca aat atc att act aca gag gac      1549
Arg Ile Thr Gln Met Gln Arg Leu Thr Asn Ile Ile Thr Thr Glu Asp
          480                      485                      490

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att gta aca gtg gtc aca atg gtg aca aat gtt gac ttt cct ccc aaa 1597
Ile Val Thr Val Val Thr Met Val Thr Asn Val Asp Phe Pro Pro Lys
495 500 505

gaa tct agt cta tgatggtggc accgtctgta cacactgagg actgggactc 1649
Glu Ser Ser Leu
510

tgaactggag ctgctaagct aaggaaagtg cttagttgat tttctgtgtg aaatgagtag 1709

gatgcctcca ggacatgtac gcaagcagcc ccttgtggaa agcatggatc tgggagatgg 1769

atctgggaaa cttactgcat cgtctgcagc acagatatga agaggagtct aaggggaaaag 1829

ctgcaaactg taaagaactt ctgaaaatgt actcgaagaa tgtggccctc tccaaatcaa 1889

ggatcttttg gacctggcta atcaagtatt tgcaaaactg acatcagatt tcttaatgtc 1949

tgtcagaaga cactaattcc ttaaataaac tactgctatt ttttttaaat gaaaaacttt 2009

tcatttcaga ttttaaaaag ggtaactttt tattgcattt gctgttgttt ctataaatga 2069

ctattgtaat gccaacatga cacagcttgt gaatgtgtag tgtgctgctg ttctgtgtac 2129

atagtcatca aagtggggta cagtaaagag gcttccaagc attactttta cctccctcaa 2189

caaggtatac ctcagttcca cggttgttaa attataaaaat tgaaaacact aacagaattt 2249

gaataaatca gtccatgttt tataacaagg ttaattacaa attcactgtg ttattttaaga 2309

aaaaatggta agctatgctt agtgccaata gtaagtggct atttgtaaag cagtgtttta 2369

gcttttcttc tactggcttg taatttaggg aaaacaagtg ctgtctttga aatggaaaag 2429

aatatggtgt caccctaccc cccatactta tatcaagggtc ccaaaatatt cttttccatt 2489

tcaaagacag cactttgaaa accctaaatt acaagccagt agaagaaaag ctaaaacacg 2549

ctttacaaat agcc 2563

<210> 16

<211> 513

<212> PRT

<213> Homo sapiens

<400> 16

Met Gly Ala Ala Ala Lys Leu Ala Phe Ala Val Phe Leu Ile Ser Cys
1 5 10 15

Ser Ser Gly Ala Ile Leu Gly Arg Ser Glu Thr Gln Glu Cys Leu Phe
 20 25 30
 Phe Asn Ala Asn Trp Glu Lys Asp Arg Thr Asn Gln Thr Gly Val Glu
 35 40 45
 Pro Cys Tyr Gly Asp Lys Asp Lys Arg Arg His Cys Phe Ala Thr Trp
 50 55 60
 Lys Asn Ile Ser Gly Ser Ile Glu Ile Val Lys Gln Gly Cys Trp Leu
 65 70 75 80
 Asp Asp Ile Asn Cys Tyr Asp Arg Thr Asp Cys Val Glu Lys Lys Asp
 85 90 95
 Ser Pro Glu Val Tyr Phe Cys Cys Cys Glu Gly Asn Met Cys Asn Glu
 100 105 110
 Lys Phe Ser Tyr Phe Pro Glu Met Glu Val Thr Gln Pro Thr Ser Asn
 115 120 125
 Pro Val Thr Pro Lys Pro Pro Tyr Tyr Asn Ile Leu Leu Tyr Ser Leu
 130 135 140
 Val Pro Leu Met Leu Ile Ala Gly Ile Val Ile Cys Ala Phe Trp Val
 145 150 155 160
 Tyr Arg His His Lys Met Ala Tyr Pro Pro Val Leu Val Pro Thr Gln
 165 170 175
 Asp Pro Gly Pro Pro Pro Pro Ser Pro Leu Leu Gly Leu Lys Pro Leu
 180 185 190
 Gln Leu Leu Glu Val Lys Ala Arg Gly Arg Phe Gly Cys Val Trp Lys
 195 200 205
 Ala Gln Leu Leu Asn Glu Tyr Val Ala Val Lys Ile Phe Pro Ile Gln
 210 215 220
 Asp Lys Gln Ser Trp Gln Asn Glu Tyr Glu Val Tyr Ser Leu Pro Gly
 225 230 235 240
 Met Lys His Glu Asn Ile Leu Gln Phe Ile Gly Ala Glu Lys Arg Gly
 245 250 255
 Thr Ser Val Asp Val Asp Leu Trp Leu Ile Thr Ala Phe His Glu Lys
 260 265 270
 Gly Ser Leu Ser Asp Phe Leu Lys Ala Asn Val Val Ser Trp Asn Gln
 275 280 285
 Leu Cys His Ile Ala Glu Thr Met Ala Arg Gly Leu Ala Tyr Leu His
 290 295 300
 Glu Asp Ile Pro Gly Leu Lys Asp Gly His Lys Pro Ala Ile Ser His
 305 310 315 320

Arg Asp Ile Lys Ser Lys Asn Val Leu Leu Lys Asn Asn Leu Thr Ala
 325 330 335
 Cys Ile Ala Asp Phe Gly Leu Ala Leu Lys Phe Glu Ala Gly Lys Ser
 340 345 350
 Ala Gly Asp Thr His Gly Gln Val Gly Thr Arg Arg Tyr Met Ala Pro
 355 360 365
 Glu Val Leu Glu Gly Ala Ile Asn Phe Gln Arg Asp Ala Phe Leu Arg
 370 375 380
 Ile Asp Met Tyr Ala Met Gly Leu Val Leu Trp Glu Leu Ala Ser Arg
 385 390 395 400
 Cys Thr Ala Ala Asp Gly Pro Val Asp Glu Tyr Met Leu Pro Phe Glu
 405 410 415
 Glu Glu Ile Gly Gln His Pro Ser Leu Glu Asp Met Gln Glu Val Val
 420 425 430
 Val His Lys Lys Lys Arg Pro Val Leu Arg Asp Tyr Trp Gln Lys His
 435 440 445
 Ala Gly Met Ala Met Leu Cys Glu Thr Ile Glu Glu Cys Trp Asp His
 450 455 460
 Asp Ala Glu Ala Arg Leu Ser Ala Gly Cys Val Gly Glu Arg Ile Thr
 465 470 475 480
 Gln Met Gln Arg Leu Thr Asn Ile Ile Thr Thr Glu Asp Ile Val Thr
 485 490 495
 Val Val Thr Met Val Thr Asn Val Asp Phe Pro Pro Lys Glu Ser Ser
 500 505 510

Leu
